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2191 AAAAATGTAACCACTTCCAAACCGCGGATGAAGATATCAAGAGT 2240
246 .LeuSerIlePheGluSerGluSplysGlyAspLysTyrAsnLysGlyT 262
2241 TCTTGGGCTTCCCAATACACATCAAGACAGCTTCAAT.....T 2284
262 yrgLnsInLeuLeuSerGlyLysValProThrLysProProthPro 278
2285 ATCAACACACCCGTGAATTAGCA...GTTCCTGTTACACTCAAGAAAA 2331
279 GlyAspProMetProProAsnGlnProGlnThrSerVal..... 293
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294 ....LeuIleArgLysTyrAlaIleGlyAspTyrSerLysLeuGlu 309
2382 AAAAGTATCAAAAATTTCTTCAGGTGAG.....AAAACCTTGTGG 2425
309 LysAlaThrLeuGlnLeuThrGlyAspAsnValAsnSerPheGlnAlaArg 325
2426 GACCGCTTGTGAATGAGTGTAATAATGT.....CAACACACA 2466
326 ValPheSerSerAsnAsp.....IleGlyGluArgIleGlu 338
2467 TTAGTGGACAATTAAGATGTACTATTCTTCACAAAGATGTGCGCT 2516
338 userAspGly...ThrTyrThrLeuThrGluLeuAsnSerProAlaGlyT 354
2517 ACMAAAGGGGAACGCTATACATTACTGAAAGTAAGCACTGCACAGAC 2566
354 ySerIleAlaGluProIleThrPheLysValGluAla.....Gly 367
2567 ATGAGTTAGCAAGAAAACGACTGGCAAAVTGAGTGAGTGAACAGGC 2616
368 LysValLysThrIleLeuSplysGlnIleGluAsnProAsnLysGly 384
2617 AAAGTA....AGCATCGATGACCAAGAAAGTACCAATCAAGT 2660
384 uIleValGluProTyrSerValGluAlaTyrAsnAspPheGluGluPhe 401
2661 TATT.....CCATTGCAAAATTGAA.....AATAATTTCTTCTTGGC 2688
401 eVal.....LeuThrThrGln.....AsnTyr 408
2699 CAATCAGAAATTAGAAATACACCATGCAAAATGGCAACAAGTAACTTA 2748
409 AlaLysPheTyrTyrAla.....LysAsnLysAsnLysSerGly 422
2749 GCAGAGCGCAGCTTTTGGCTTGCAAAAGAAAAATGCTCAAGAAATTACCA 2798
422 nValValTyrCysPheAsnAlaSplysSerProProAspSerGlu 439
2799 AACTGTGGCAACTCAAAAAACAGAT..... 2823
439 sPcLysGlyLysThrMetThrProAspPheThrGlyGluValLysTyr 455
2824 .....ACTACAGA..... 2832
456 ThrHisIleAlaGlyArgAspLeuPheLysTyrThrValLysProAlaArg 472
2832 ..... 2832
472 pThrAspProAspThrPheLeuLysHisIleLysLysValIleGluLysG 489
2833 .....TTGAGCTATTTT...AAAATTAAGTGAACCTG 2860
489 Lys...TyrArgGluLysGlyGlnAlaIleGluLysSerGlyLeuThrGlu 504
2861 GTGAGATTCGA.....ATGCTGGAACAATCAGCA..... 2889
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2890 ....CCATTAGGTAGACACTCTTGTGGAATATGAAATTTACT..... 2931

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2950 .....ATTCACTATGCGAGGC 2964
555 .....AspSerAsnProProGlnLeuThrAspLeuAspPhePheIle 568
2965 AAAAATATTGAAGAAAATGGCCAGATGAGCA..... 2997
568 eProAsnAsnAsnLysTyrGlnSerLeuIleGlyThrGlnThrHisProG 585
2997 ..... 2997
585 LysAspLeuValAspIleIleArgMetGluSplysGluValIlePro 601
2997 ..... 2997
602 ValThrHisAsnLeuThrLeuArgLys.....ThrValThrGlyLe 615
2998 CTGACACATCAAAATATTTGAAACCTTTGACTTACACTTATATAAAA 3047
615 uAlaGlyAspArgThrLysAspPheHisPheGluIleGluLeuLysAsn 632
3048 AGCGGATTAATCAGACG.....CCACTTAAAGAG 3076
632 snLysGlnGluLeuLeuSerGlnThrValLysThrAspLysThrAsnLeu 648
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649 GluPhe...LysAspGlyLysAlaThr.....IleAsnLe 659
3112 GAATTCACAAAGATGGCAAGAAACGATCTTGTGTTTGAACAACTT 3161
659 uLysHisGlyGlu...SerLeuThrLeuGlnGlyLeuProGlyLys 675
3162 AAAACAGGAAATATGTTCTTACAGAAACCTTACGCCAGAGATATC 3211
675 eTyrLeuValLysGluThrAsp.....SerGluGlyTyrLysVal 688
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689 LysValAsnSerGlnGluValAlaAsnAlaThrValSer.....Lys 702
3262 ACGATAGATGGGAAAGATGACGATGTTTAATTTCTGAGAGAAAGA 3311
702 sThrGlyIleThrSerAspGluThrLeuAlaPheGluAsnAsnLysGluP 719
3312 TAATCAAAATTACTTTAGACGTAG.....AACCAAGCAAAAGGTTG 3352
719 roValValProThrGlyValAspGlnLysIleAsnGlyTyrLeuAlaLeu 735
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; Sequence 45, Application us/09070927
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; APPLICANT: Patrick J. Dillon
; APPLICANT: Steven C. Barash
; TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and
; NUMBER OF SEQUENCES: 982
; CORRESPONDENCE ADDRESS:

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10112 .....AAATAGTGAACCTGTGATGCA..... 10138
496 Alalleglutyrseryleuthrcluthrcluthrcluthrcluthrcl 512
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10177 TGGCGAAATTATGATTACT.....GTGATATA..... 10207
529 eulysaspyrthsglypneglyaspmetasnaspserthleualaval 545
10208 .....TATGGGAAA..... 10216
546 Alalyslleuvalglutyralagl.....Aspserasnpropr 559
10217 .....ATTCACTATGCGCAAAATTTGAAAGAAATGCGCC 10254
559 OGlnleuthraspleuasphepelleproasnasnulystyrglns 576
10255 AGATGAGCA..... 10264
576 erleuileglythgltrphtisprogluaspuleuvalaspillearg 592
10264 ..... 10264
593 Metgluaspyspysgluvalilleprovalthrhisasnleuthrleax 609
10265 .....CTGACACATCAAAATTAATTGAA 10287
609 glys.....ThrvAlthrGlyleuAlaglyAsparthrlyasp 623
10288 ACCGTTTGACTTACAGTTATAAAAAAGCGATATCAGACG..... 10330
623 hehispegluilegluleuylsasnulysglnleuLeuSergln 639
10331 .....CCACTTAAAGAGCGAAATTCGTTTAAACAGCA... 10363
640 ThrValysThrAspLysThrAsnleuGluPhe..LysAspGlyLysAl 655
10364 .....CCAGATACGGATATTGAATTACCAAAAGATGCCAAGA 10401
655 arhr.....IleasnleuLysHISglnu...SerLeut 666
10402 AACGGATACCTTTGTTTGAACCTTAAACAGGGAATATGTTCTAA 10451
666 hrlenginglyleuproglylytyrsertyrleuValLysgluthrAsp 682
10452 CAGAAACCTTTACGCCAGAGATATCAGGGGTAAACCAATCGAA 10501
683 .....SerglulglytyrlyvallyvalysnserglnluvalAl 696
10502 TTAATAATTCGTGAAGATGTTCACTACGATAGTGGGAAAAAGTAGC 10551
696 aasnulatThrValser.....LysThrGlyLleThrserspglut 710
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710 hrlenualaphnegluasnulysgluProvalValProthrGlyValasp 726
10602 CG.....AACCAAGCAAAAGGTTCTTACCTGAACAGTGGGCATA 10642
727 GlnLyslleasnnglytyrleuAlaleuile.....Valilleagl 740
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740 Yliserleuglyle 745
10693 TGTATTATCTTTATT 10708
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; Sequence 45, Application US/09070927A
; GENERAL INFORMATION:
; APPLICANT: Charles A. Kunsch
;          Patrick J. Dillon
;          Steven Barash
; TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 982
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,927A
; FILING DATE: 04-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/046,655
; FILING DATE: 1997-05-16
; APPLICATION NUMBER: 60/044,031
; FILING DATE: 1997-05-06
; APPLICATION NUMBER: 60/066,009
; FILING DATE: 1997-11-14
; ATTORNEY/AGENT INFORMATION:
; NAME: Kenley K. Hoover
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PB369
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15614 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-070-927A-45

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127 YrlsLysHISAspGlyLleSerThrLysPheGluasp..... 139
9143 ATCAAGTAGCT.....ATTCAAACAGAGTCAGAAACTTCAAACTGAT 9186
140 .....TyralaMetSerProvalGlyleThrGlyAspGluLeuasnGlnly 154
9187 TTTTGTATCAAAATGAATGTCGACAAACGTTTCAGCCATTAGCCACAGCG 9236

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  sequence 1048, Application US/60045649
  GENERAL INFORMATION:
    APPLICANT: Lagace, Robert E.
    APPLICANT: Corely, Neil C.
    APPLICANT: Russo, Frank D.
    APPLICANT: Hann, Amy L.
    TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF ENTEROCOCCUS FAE
    NUMBER OF SEQUENCES: 1466
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
    STREET: 3174 PORTER DRIVE
    CITY: PALO ALTO
    STATE: CALIFORNIA
    COUNTRY: USA
    ZIP: 94304
    COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
    CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/60/045,649
    FILING DATE:
    CLASSIFICATION:
    ATTORNEY/AGENT INFORMATION:
      NAME: GERONE, MICHAEL C.
      REGISTRATION NUMBER: 39,132
      REFERENCE/DOCKET NUMBER: PM-0003P
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (415) 855-0555
      TELEFAX: (415) 845-4166
    INFORMATION FOR SEQ ID NO: 1048:
      SEQUENCE CHARACTERISTICS:
        LENGTH: 7971 base pairs
        TYPE: nucleic acid
        STRANDEDNESS: single
        TOPOLOGY: linear
        MOLECULE TYPE: cDNA
        IMMEDIATE SOURCE:
        CLONE: EF1c1048
      US-60-045-649-1048

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110 neuylslsAlaPheProleuGlySerAspSerSerValyslslsTPrT 127
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1741 2522
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399	GIUHPSErSeV..	LeuHrHrGrIn	406
2561	TCCTTGGCCAAATGAGATTGAAAATATACACCTGACAAAATGGCCAAACAACT			2610
407	.AsnYrAlaLysPheTyTYrAla	LysAsnLysAsnLys	420	
2611	GAACCTTAGCAGAGGCGACTTTCGCTTGCCAAAGAAAATAATGCTCAAGGAA			2660
420	eSeSergInValValTYrCYSPheAsnAlaAspLeuLysSeSPrProAsp	LysSeSPrProAsp	436	
2661	GTTACCAACAACTGTGGCAACCTCAAAAACAGAT	2692	
437	SeSGLysAspGLYGLYsHrHrmetHrProAsPheHrHrInGLYLuVa	453
2693	ACTACAGCA	2701
453	LysTYrHrHrHisILeAlaGLYAspLeuPheLysTYrHrValLysP	2701	
470	roAspAsPheAsPheAsPheAsPheLysHisILeLysValILe	486	
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487	GIuLYsGLY...TYrArGLYsGLYsGLYsInAlaILeGLYrSeSGLYLe	502	
2723	GAACCTGGAGAGATACGA	ATGGCGAACAATCAGGA	2758
502	uHrGLuHrGLInLeuAlaAlaILeHrGLInLeuAlaILeTYrTYrPheT	519	
2759	CCATTAGGCTACGACACCTCTTGCGAAATTAAGATTTA	2798	
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552	rAlaGLIn	AsPheAsnPrProGLInLeuHrAsPheAsnPr	566
2827	TGCAGCGAAAAATATTGAGAAATGCCGCCAAATGGCA	2866	
566	hePheILeProAsnAsnAsnLysTYrGLInSeSLeuILeGLYHrGLInPr	582	
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583	HisPrOGLInAsPheuValAsPheILeLerGmetGLYAsPheLysGLYLuVa	599	
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599	ILePrOVALThrHisAsnLeuThrLeuArGLYs	ThrValT	613	
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2910	ATPAAAAAACCATATATGACAGC	CCACCTT	2938	
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2939	AAAGAGCCAAATTCGCTTTAACAGCA	CCAGATAC	2973	
646	rAsnLeuGLYrHe	LysAsPGLYsAlaThr	657
2974	GCATATTGAATTACCAAAAGATGCGAAAGAAACGATACTTTGCTTTTTCG	3023	
657	LeAsnLysHisGLYLuIn	SeSLeuThrLeuGLInGLYLeuPrOGLIn	672
3024	AAACCTTAATAACCGAGGAATATGTGTTTACCGAACAACCTTTACGCGAADA	3073	

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686 rDysValysValasSergIngluValAlasnaLaThrValSer.... 701
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3124 TTCACGTACAGATAGATGGGAAAAGTAGACAGATCTTTAATTCTCGAG 3173
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sequence 1042, Application US/6004653
GENERAL INFORMATION:
APPLICANT: Lagace, Robert E.
APPLICANT: Corley, Nell C.
APPLICANT: Russo, Frank D.
APPLICANT: Hann, Amy L.
APPLICANT: Heath, Joe D.
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF ENTROCOCCUS FAECALIS
TITLE OF INVENTION: GENOME, FRAGMENTS THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 1449
CORRESPONDENCE ADDRESS:
ADDRESS: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/60/046,653
FILING DATE: HERewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CERONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PM-0003-1 P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 855-4166
TELEFAX: (415) 845-4166
INFORMATION FOR SEQ ID NO: 1042:
SEQUENCE CHARACTERISTICS:
LENGTH: 8040 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: EFALIG1042
US-60-046-653-1042
alignment_scores:
Quality: 192.00 Length: 716
Ratio: 0.598 Gaps: 45
Percent Similarity: 44.832 Percent Identity: 23.603
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alignment_block:
US-09-494-297-2 x US-60-046-653-1042 ..

Align seg 1/1 to: US-60-046-653-1042 from: 1 to: 8040

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1908 CCTGAAAGAGTTGATTT.....GGGCTTC 1933
171 etGlnGlyLeuGluProLeuAsnAlaIleArgValThrGlnAlaVal 187
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1934 CTTCGGGAAAAGCACCT.....GGCTGAAGTTAAACGTAAAAAATC 1977
188 TrpTyrTyrSerAspAsnAlaProIleSerAsnProAspGluSer.Phe 204
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243 sprPheGlnLeuSerIlePheGluSerGluAspLysGlyAspLysTyrAsn 259
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2177 .....TTCCTGGGCTTCCCAATATACCAATCAAGAGCAAGCTTTCAT 2221
260 LysGlyTyrGlnAsnLeuLeuSerGlyLysValProThrLysProPr 276
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276 oThrProGlyAspProMetProMetProAsnGlnProGlnThrThrSerV 293
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293 al.....LeuIleArgLysTyrAlaIleGlyAspTyrSerLysLeu 306
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2313 TAGATTAAAGTAAATCAAAAATTTCTTCAGGTGAG.....AAAAAC 2356
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352 AlaGlyTyrSerIleAlaGluProIleThrPheLysValGluAla.... 366
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2498 GCAGACATAGCTTAGGCAAGAAACGACTGGCAATTTAGGTAGTCA 2547
367 ....GlyLysValTyrThrIleLeuAspGlyLysGlnIleGluAsnPro 382
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2548 GCAAGCGCAAGTA....AGCATCGATGACAAAGAGTACCACCAACAA 2591
382 snLysGluIleValGluProTyrSerValGluAlaTyrAsnAspPheGlu 398
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2592 ATCAAGTTATT.....CCATTGGAAATGAA.....AATTAATTTTCT 2629
399 GluPheSerVal.....LeuThrThrGln..... 406
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2630 TCTTTGCCAATCAGAAATTAGAAATACCATGCAAAATGCAACAAGT 2679
407 .AsnTyrAlaLysPheTyrTyrAla.....LysAsnLysAsnGly 420
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2680 GAACCTTAGCAGAGCGCACTTTGGTTGCAAGAAAAAATGCTCAAGAA 2729
420 erSerGlnValValTyrCysPheAsnAlaAspLeuLysSerProProAsp 436
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2730 GTTACCAAACTGTGCACTCAAAAACAGAT..... 2761
437 SerGluAspGlyLysThrMetThrProAspPheThrThrGlyGluVa 453
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2762 .....ACTACAGA..... 2770
453 LysTyrThrHisIleAlaGlyArgAspLeuPheLysTyrThrValLysP 470
2770 ..... 2770
470 roaArgAspThrAspProAspPheThrPheLeuLysHisIleLysValIle 486
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2771 .....TTGAGCTATTTT...AAATATAGT 2791
487 GluLysGly...TyrArgGluLysGlyGlnAlaIleGluTyrSerGlyLe 502
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2792 GAACCTGTGATGATCA.....ATGGTGGACACACAGAA... 2827
502 uThrGluThrGlnLeuArgAlaThrGlnLeuAlaIleTyrTyrPheT 519
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2828 .....CCATTAGCTACGACACTCTTGGTGAATATGAAATTTTA 2867
519 hrAspSerAlaGluLeuAspLysAspLysLeuLysAspTyrHisGlyPhe 535
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2868 CT.....GTGATTA.....TAT 2881
536 GlyAspMetAsnAspSerThrLeuAlaValAlaLysIleLeuValGluT 552
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2882 GCGAAA.....ATTCACTA 2895
552 rAlaGln.....AspSerAsnProProGlnLeuThrAspLeuAsp 566
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2896 TGCAGCGCAAAATATTGAAGAAATGCGCAGATGAGCA..... 2935
566 hePheIleProAsnAsnLysTyrGlnSerLeuIleGlyThrGlnTrp 582
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2935 ..... 2935
583 HisProGluAspLeuValAspIleIleArgMetGluAspLysGluVa 599
2935 ..... 2935
599 lIleProValThrHisAsnLeuThrLeuArgLys.....ThyValT 613
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2936 .....CTGACACATCAAAATATTGAAGAACTTTGACTTAACAGTTC 2978
613 hrGlyLeuAlaGlyAspArgThrLysAspPheHisPheGluIleGluLeu 629
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2979 ATAAAAAGCCGATATACAGCG.....CCACTT 3007
630 LysAsnAsnLysGlnGluLeuSerGlnThrValLysThrAspLysTh 646

```



```

Align seg 1/1 to: US-09-663-779-1301 from: 1 to: 10627

208 GluSerAsnLeuValSerThrSerGlnLeuSerLeuMetArgGlnAlaLe 224
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
3989 GAAATGAAATGATGGATACAGCAATGTACAGATA..... 4024
224 uLysGlnLeuLeuAspProAsnLeuAlaThrLysMetProLysGlnValP 241
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4025 .....ACAAAATAGATTAAGATAGTA 4046
241 roAspAspPheGlnLeuSerIlePheGlnSerGluAsp...LysGly... 255
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4047 AAGCTCATTTGAAAAATGTTGATTTTGAAGTACGCTGATTTAAAGGAAAA 4096
256 .....AspLysThrAsnLysGlyTyrGlnAsnLe 265
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4097 GTAGTGCAAAAGTACAGCAGATAAAGAAAGAAACCAACGTTTCAGA 4146
265 uLeuSerGlyGly.....LeuValProThrLysProProThrProG 279
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4147 TTATATCTATTTGGAAGTATGAGTATGAGAAAGTAAACACCGGACAGAT 4196
279 LysAspProPheProAsnGlnProGlnThrThrSerValLeuIle 295
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4197 ACAACACACTAGAAAGCCAAATTCATTCGAAATTTGAAAGGTAAGATA 4246
296 ArgLysTyrAlaIleGlyAspTyrSerLysLeuGlnGlyAlaThrLe 312
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4247 ACACCATTTACAAATTGACTGTAGAAATGAATTTAGTGATACAGAAATGT 4296
312 uGlnLeuThr.....GlyAspAsnValAsnSerPheGlnAlaArgV 326
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4297 AGAAATTACAAAGTAGATAAAGAAATTAAGATGCTTACCTGATGCG 4346
326 alPheSerSerAsnAspIleGlyGluArgIle..... 336
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4347 TCTTGGAAATTCAGATGAAACAGACAGACAGTACGCTAAATTAACACA 4396
337 .....GlnLeuSerAspGlyThrTyrTh 344
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4397 GATTAATAAGACACAAAGCAAGTACTATTATTCAGTCGACATACAA 4446
344 rLeuThrGlnLeuAsnSerProAlaGlyTyr...SerIleAlaGluProI 360
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4447 GTTAGTGAAGTAAAGCACCAAAAGATTAACAATGTAGATATCGA 4496
360 LeuThrPheLysValGluAlaGlyLysValTyrThrIle.....Ile 373
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4497 TTACTTTCCAAATTTGAAAGGCGCATGACAAATCTCTTGCTTTACAGTA 4546
374 AspLysLysGlnIleGluAsnProAsnLysGluLe.....ValGluPr 388
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4547 GAAACGAAATGTAGACAAAGGAAATGTGGAAGTAAACAAAGTAGATAA 4596
388 ctyrSerValGluAlaTyrAsnAspPheGlnGluLupheserValLeuThrT 405
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4597 AGATAGTCAAAAAGCATTA..... 4615
405 hrgIAsnTyrAlaLysPheTyrTyrAlaLysAsnLysAsnGlySerSer 421
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4616 .....GCA 4618
422 GluValValTyrCysPheAsnAlaAspLeuLysSerProProAspSerG 438
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4619 AGTGTAGCTTC.....GAAGTACACAGA 4641
438 uAspGlyGlyLysThrMetThrProAspPheThrThrGlyGluValLysT 455
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4642 CGAACCAAGGCAAGTAGTAACA...GAAGTACAGCAGATTAAGAACAGCA 4688
455 ytrThrHisIleAlaGlyArgAspLeuPheLysTyrThrValLysProArg 471
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4689 AAGCAAAATCTCAGACTATCTGTAGGAAGTAC..... 4723
472 AspThrAspProAspThrPheLeuLysHisIleLysLysValIleGlyL 488
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4724 .....AAATAGTAGAGAA 4737
488 S.....GlyTyrArgGluLysGlyGlnAlaIleGluTyr.... 499
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4738 AAAAAGCTTACAGGTATACAAAAAATACAGACAGCCAGTATCATTCGAAA 4787
500 .....SerGlyLeuThrGluThr...GlnLeuArgAlaAlaThrGlnLeu 513
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4788 TTAAGAGGCTATGACAGAGCTTATCATTTAAAGTAGAAGAAAGAACAG 4837
514 AlaIleTyrTyrPheThrAspSerAlaGlnLeuAspLysAspLysLeu 530
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4838 TTAGACAAAGCTTTAGTAGAAATCACAAAAGTAGATTAAGATAGTCAAAA 4887
530 sAspTyrHisGly.....PheGlyAspMetAsnAspSerThrLeuAlaV 545
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4888 AGTATTAGAAGCGTAGCTTCTCGAAGTACAGATGAAAGCAAAAGTAG 4937
545 alAlaLysIleLeuValGluTyrAlaGlnAspSerAsnProProGlnLeu 561
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4938 TAACAAAAGTACACACAGAT.....AAAGAAAGCAAAAGCAAGATT 4978
562 ThrAspLeuAspPhePheIleProAsnAsnAsnLysTyrGlnSerLeuI 578
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4979 GCTGATTTATTCAGTA.....CGAAATATATAG...CTAGT 5010
578 eGlyThrGlnThrHisPro.....GluAspLeuValAspIleLeuArgM 593
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5011 AGAGGTAGAGCGTACCAGATATAAAACTAGCAAAACCACTACAT 5060
593 etGluAspLysLysGluValIleProValThrHisAsnLeuThrLeuArg 609
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5061 TTGGAATCCAAAAA.....GCTATGACAGAGACTTATTCCTTAATA 5101
610 .....LysThrValThrGlyLeuAl 616
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5102 GTAGAGATGAATAGTAGACAAAGGCTCAGTAGAAATCAACAAAAGTGA 5151
616 agLysAspArgThrLys.....AspPheHisPheGlnIleGluLeuL 630
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5152 TAAAGATAGTCAAAAAGTATTAGAAGACGTAGTCTGCAAGTCA... 5197
630 ysaAsnAsnLysGlnGluLeuLeuSerGlnThrValLysThrAspLysThr 646
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5198 ....GACGACAAAGGAAAGTACTAACGCAAGTAAACAGAT..... 5236
647 AsnLeuGlnPheLysAspGlyLysAlaThrIleAsn..... 658
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5237 .....AAAATGGTAAAGCAAAAATCTCAGACTTATCTGAG 5274
659 .....LeuLysHisGlyGlnSerLeuThr...LeuGlnGlyLeuP 671
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5275 AAAGTACAAATTTAGTAGAAAGAGCTTACAGGCTACAAAAAACTAA 5324
671 roGluGlyTyrSerTyrLeuValLysGlnThrAspSerGlnGlyTyrLys 687
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5325 CAGAGCCAGTATCATTCGAAATTTAAAAAGGCTATGACAGAGAGTGTATCA 5374
688 ValLysValAsnSerGlnGluValAlaAsnAlaThrValSerLysThrG 704
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5375 TTAAGATAGAGATGAACAGTTAGCAAAAGTTCAGTAGAAATACACAA 5424
704 yIleThrSerAsp.....GluThrLeuAlaPheGlu... 714
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5425 AGTAGATTAAGATAGTCAAAAAGTATTAGAAAGCGGTCTTCACAGTAC 5474
715 ...AsnAsnLysGluProValValProThrGlyValAspGlnLysIleAsn 730
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5475 AAGCGACAAAGCAAGTAGTA...ACAGAGTAAACAGATAAAT 5521

```



```

; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: genomic DNA
; IMMEDIATE SOURCE:
; CLONE: EFM1c748
; US-60-068-186-748

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alignment_scores:

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Quality: 180.00 Length: 741
Ratio: 0.347 Gaps: 41
Percent Similarity: 44.399 Percent Identity: 20.783

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alignment_block:

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US-09-494-297-2 x US-60-068-186-748 ..

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Align seg 1/1 to: US-60-068-186-748 from: 1 to: 18768

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72 TrpTyr.....GlyTyrGluSerTyrValArgGlyH1 82
|||||
12459 TGTACACTTTCAGTCAAGAGTGGGACAGACCTTAC...AACGGTCA 12505
82 s.ProTyrTyrLysGlnPheArgValAlaHisAspLeuArgValAsnLeu 98
|||||
12506 CTCCA.....TCTATTTCCTA 12522
99 GluLysSer.....ArgSerTyrGlnValTyrCysPheAsnLeuLysLys 113
|||||
12523 GAAGGAATATCCATCAAGACATCAGATCTAT..... 12555
113 AlaPheProLeuGluLysSerAspSerValLysLysTyrTyrLysLysH 130
|||||
12556 .....TTAGAAAGACCAAGAAATCCAAATCCATTACCAAGTGA 12595
130 IsAspGlyLysSerThrLysPheGluAspTyr..... 140
|||||
12596 GA.....ATCCAAACAGAAATGAGAGCTCCATCCAAATTCGTGAT 12639
141 .....AlaMetSerProArgGlyLeuThrGlyAspGluLe 151
12640 CAATGACGAGCAGACACACTTTCAGCCAAACATTGATACCAATGAAAT 12689
151 uAsnGlnLysLeuArgAlaValMetTyrAsnGlyHisProGlnAsnAla 168
|||||
12690 AGCTGAA.....T 12697
168 snGlyIleMetGluGlyLeuGluProLeuAsnAlaIleArgValThrGln 184
|||||
12698 TCGGTATACCATCTGCTAAGCTCCGAGTCACTTCACATC..... 12741
185 GluAlaValTyrTyrTyrSerAspAsnAlaProLysSerAsnProAspG 201
|||||
12742 AAAAAGTTATGGGAAGATTGACACAAATCTACCTGATCGTCAAGATCA 12791
201 u.....SerPheLysArgGluSerGluSerAsnLeuValSerThrSerGln 217
|||||
12792 AGTACACTTTGAGATTCACGCGAA.....CATACGACAAATG 12829
217 euSerLeuMetArgGlnAlaLeuLysGlnLeuIleAspProAsnLeuAla 233
|||||
12830 CTGCAGCTTGGAAAAAGGATATATTCGAATCAATTAACCGATTAAGAT 12879
234 Thr.....LysMetProLysGlnVal 240
|||||
12880 ACAACAATACGTGGGAACGTGACACATTGACAAATATATCTGCAAAATAG 12929
240 LProAspAspPheGln.....LeuSerIlePheGluSerGluAspLysG 255
|||||
12930 CGGAGAAAGTATCATCAGAGATATATCTACCTCAATATACATATATCAG 12979
255 LysAspLysTyrAsnLysGlyTyrGlnAsnLeuLeuSerGlyGlyLeuVal 271
|||||
12980 GTCAAGCATTCAGT.....TACCAACAATC..... 13005

```

```

272 ProThrLysProProThrProGly.....AspProPr 282
|||||
13006 ...AAAGAAATACCTGTACCAAGGATACGATTCACAAATAGATGCAAT 13052
282 oMetProProAsnGlnProGlnThrThrSerVal.....LeuIleA 296
|||||
13053 GACATGGAAAAATATCAACAAATTCACACCGCTTAACCTGAAAAATACGA 13102
296 rGlyTyrAlaIleGlyAspTyrSerLysLeuGluGlyAlaThrLeu 312
|||||
13103 AAAATTCCTCTGCAGGTGA.....AAGATTCATCGGCTGTCTTC 13146
313 GlnLeuThrGlyAspAsnValAsnSerPheGlnAla...ArgValPhe 328
|||||
13147 AAATTAACAGAGATTCCTATTGATCTTACTACTACATCATGCGACGCG 13196
328 rSerAsnAspIleGlyGluArgIleGluLeu...SerAspGlyThrTyr 344
|||||
13197 AACCTATTCCTCTCCAGAAAAATGCAAAATTCAGAAAAATGACCTATA 13246
344 hLeuThrGlnLeuAsnSerProAlaGlyTyrSerIleAlaGluProIle 360
|||||
13247 CGCTGACAGAAACAAAGCTCCAGACAGCGCATTAACGAAAAAGACT 13296
361 ThrPheLysValGluAlaGlyLysValTyrThrIle...IleAspGlyLys 376
|||||
13297 ACTTGGGAAATCAAGATCCGCTTCGTGATGTAGCGTAAACCTGATGAAA 13346
376 s.....GlnIleGluAsnProA 382
|||||
13347 AACAGTCACTACTCCGATGATACGATCCAGTTGATGATGAAATCCTT 13396
382 snLysGluIleValGluProTyrSerValGluAlaTyrAsnAspPheGlu 398
|||||
13397 TTGTTGAAGTT.....CCTGTACAGTACGTAAAGTATGCGATCAAGCG 13440
399 GluPheSerValLeuThrThrGlnAsnTyrAlaLysPheTyrTyrAlaLys 415
|||||
13441 ACGGACAAAGATTAATCTTAAGAGACGACATTTCCCTACGAAAAA 13490
415 sAsnLysAsnGlySerSerGlnValValTyrCysPheAsnAlaAspLeu 432
|||||
13491 AGAAGCAAAATGTACTATTCG..... 13512
432 ySerProProAspSerGlu.....AspGlyGlyLysThrMetThr 445
|||||
13513 ....CCAATTGACAGCCAAACAAAGAAATGAAAAAGCTTGGCCAGTTT 13557
446 ProAspPheThrThrGlyGluValLysTyrThrHisIleAlaGlyArgAs 462
|||||
13558 GATTCACCTACACCTGTAATATATCGAGTGTGAACAGCTGCTCTGC 13607
462 pLeuPheLysTyrThrValLysProArgAspThrAspProAspThrPhe 479
|||||
13608 CGGATAT.....GATACCTCCCGGGAATATATG 13636
479 euLysHisIleLysLysValIleGluLysGlyTyrArgGluLysGlyGln 495
|||||
13637 AATTCCAAATGATTAATAT.....GGAAAA 13662
496 AlaIleGluTyrSerGlyLeuThrGluThrGlnLeuArgAlaAlaThrG 512
|||||
13663 ATCATTT...TACACGGGAAAAAATACGAGATGACAAATATATATGAGAC 13709
512 nLeuAlaIleTyrTyrPheThrAspSerAlaGluLeuAspLysAspLys 529
|||||
13710 GCTCAGCATCAAAATGACATTAAGGCTTTGATGATCAACGTTACACAAA 13759
529 euLysAspTyrHisGlyPheGlyAspMetAsnAspSerThrLeuAlaVal 545
|||||
13760 AAGAAGAC.....AACGACAGACATTTAAAGA 13788

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546  AAlaYsIleLeuValaIGlTyrAlaIlnAspSerAsnProPogIlnLeuTh 562
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13789  GCAAAATTTCAGACTGCAG.....GCACCAAGAATG.. 13818
562  rAspLeuAspPhePheIleProAsnAsnAsnLysTyrGlnSerLeuIleG 579
      |||||:::
13819  .GACTTAGAATTG..... 13830
579  lYThGlnTrpHisProGlnAspLeuValAspIleIleArgMetGlnAsp 595
      |||||:::
13831  .....CCAAAGAT..... 13839
596  LysLysGluValIleProValTrpHisAsnLeuTrpLeuArgLysThrVa 612
13839  ..... 13839
612  lThrGlyLeuAlaGlyAspArgTyrLysAspPheHisPheGluIleGluL 629
      |||||:::
13840  .....GGACAAGAAACAGATACCTTTCTATTCCAA..... 13869
629  euLysAsnAsnLysGlnGluLeuLeuSerGlnThrValLysThrAspLys 645
13869  ..... 13869
646  ThrAsnLeuGluTrpPheLysAspLysAlaThrIleAsnLeuLysHisG1 662
13870  .....AATTAAACCTGG 13883
662  yGlu...SerLeuTrpLeuGlnGlyLeuProGluGlyTyrSerTyrLeu. 677
      |||||:::
13884  AACTATACGCGTACCCGAACTTTTACACGCAAGAGATACCAAGTCTAA 13933
678  .....ValLysGluThrAspSerGlnGlyTyrLysValLysValAsn 691
      |||||:::
13934  AAGAGCCAGTACTACTAGTATACGCAAGATGGGTCAATTCAAGTGAT 13983
692  SerGlnGluValAlaAsnAlaThrValSerLysTrpGlyIleTrpSerAs 708
      |||||:::
13984  GGACAAAGAT.....CATGAATCTGTTCTGTGCACCGAGGACCCAAACAA 14027
708  pGlu...ThrLeuAlaPheGluAsnAsn...LysGluProValValProT 723
      |||||:::
14028  CCAGATTCTTTAGACATCAGACATCAGCAAAAGTACCATTACTGTGAA 14077
723  hrGlyValAspGlnLysIleAsnGlyTyrLeuAlaLeuIleValIleAla 739
      |||||:::
14078  CGGAGGAATGGCCGCTTAGGAATCTAT.....CTAGTAGGATGATT 14121
740  GlyIleSerLeuGlyIleTrp 746
      |||||:::
14122  GGTGTGCGTTTCTATTATTTGG 14142

seq_name: /cgn1_7/prodata/./pna/US6005_COMB.seq:US-60-050-444-744

seq_documentation_block:
  Sequence 744, Application US/60050444
  GENERAL INFORMATION:
    APPLICANT: APPLICANT:lagace, Robert E.
    APPLICANT: Corley, Neil C.
    APPLICANT: Russo, Frank D.
    APPLICANT: Hann, Amy L.
    APPLICANT: Heath, Joe D.
    TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF ENTEROCOCCUS FAECALIS
    TYPE OF INVENTION: GENOME, FRAGMENTS THEREOF, AND USUS THEREOF
    NUMBER OF SEQUENCES: 1063
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
    STREET: 3174 PORTER DRIVE
    CITY: PALO ALTO
    STATE: CALIFORNIA
    COUNTRY: USA
    ZIP: 94304

COMPUTER READABLE FORM:

```

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2.2
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/60/050,444
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: CERRONE, MICHAEL C.
 REGISTRATION NUMBER: 39,132
 REFERENCE/DOCKET NUMBER: PM-0003-2P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 855-0555
 TELEFAX: (415) 845-4166
 INFORMATION FOR SEO ID NO: 744:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18766 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 IMMEDIATE SOURCE:
 CLONE: EPM1c744

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alignment_scores:
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Quality:	180.00	Length:	74
Ratio:	0.547	Gaps:	41
Percent Similarity:	44.399	Percent Identity:	20.783

alignment_block:
US-09-494-297-2 x US-60-050-444-7444

Align seg 1/1 to: US-60-050-444-744 from: 1 to: 18786

72 Трпуг.....GlytyrgluserTyvalargGlyni 82

12459 TGGTACACTTTTCAGTCAAGAGTGTGGGGACAAGTCTAC..AACGGTCA 12505

82 S. ProtyrtyrLysGlnPheArgValAlaHisAspLeuArgValAlaSerLeu 98

12506 CTCCA.....TCTATTTCATA 12522

99 GluGlySer.....ArgSerTyrGlnValTyrCysPheAsnLeuLysLy 113

12523 GAAGGAATACCATCAAGAGCATCAGATCTAT 12555

```
113 ca)ababroI auCl v$arbenSorSerVa)I vel vst rntvri vel vch 130
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[illegible]

```
130 lsaspoly1eserintlyspnecluaspyr..... 140
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12596 GA.....ATCCAACAGAAATGAGGACTTCATCCAAATTCTGGTAT 12639

141AlaMetSerProArgIleThrGlyAspGluLe 151

12640 CAAATGACGGCAGGACCACTTCCAGCCAAACATTGATACCAATGAATT 12689

151 uasnglnlvslvleuaraqalavajmettyrasnglvhisploglnasnaiaa 168

13690 AGCTGCA
| :::
T 13697

23

```

100      |||||          ||           ::::::::::::::
       | | | | | : : : : | | | | | : : : : : : : :
       | | | | | : : : : | | | | | : : : : : : : :
       | | | | | : : : : | | | | | : : : : ~~~~~~

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12698 TCGGATATACCACTGCTAAAGCTCCGGAGTCAGTCTTCACATC..... 12/41

185 G L A L A V A I T P T Y T Y r S e r a s p a s n a l a P r o I l e s e r a s n P r o a s p c l 201

12742 AAAAGTTATGGGAGAATTGACACAATCTAGCTGATCGTCCAGATCA 12791


```

15219 GCCA.....AAGCGGGTAAATTGACATGTAGGGCAATT 15253
188 rPtyrTyrSerAspAsnAlaPro.....IleSerAsnProAsp 200
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   |||.....:|||||:|||||
15254 GGTGTGATCTGCACCGATGCCAATAAAGCCGCAATTTTATAGATAAACAGAC 15303
201 Glu.....SerPheIysArgIleuSerGluSer 210
   :|||
   :|||.....:|||||:|||||
15304 GATTAAGATAGCGACTTATTTTAACTCAACACAGAAATCAAAAGAAAGCGCA 15353
210 nleuValSerThrSerGlnIleuSerLeu..... 219
   :|||||
   :|||||.....:|||||:|||||
15354 TTGTGGAGTGCAGCAGACACTTATCTAAACGCTTAAATATAACACA 15403
220 .....MetArgGlnAla 223
   :|||||
   :|||||.....:|||||:|||||
15404 CCGCGGCACCTATAGCGCGGACCTTGGATCAAAATACCTTAAGAAGCAA 15453
224 LeuLysGlnIleuIleAspProAsnLeuAlaThrLysMetProLysGlnIle 240
   :|||||
   :|||||.....:|||||:|||||
15454 TTGTCTTATTTATGACAAACCAACAAAGACGCGGATGGCGCTTAAAT 15503
240 LProAspAspPhe.....GlnIleuSerIleIlePhe 250
   :|||||
   :|||||.....:|||||:|||||
15504 CAGAGCTCAGTTTGGATACCGACAAAAGGTCAATGAAGCGGTGTCTATG 15553
250 LuserGlnLysPlys.....GlyAspLysTyrAsnLysGlyTyrGlnAsn 264
   |||
   |||.....:|||||:|||||
15554 AGATTGACGCCCAAGATTATATGCGAACCGCTTACGTGGCACACCAAACTT 15603
265 LeuLeuSerGlyGlyLeu.....ValProThr 273
   |||
   |||.....:|||||:|||||
15604 TTGATTGATGATTAACACACCAATACCGCACCTTTGTTAAAGACCTGTCTTC 15653
273 rLysProProThrProGlnIleAspProIleProIleProIleProIleProGln 290
   :|||||
   :|||||.....:|||||:|||||
15654 CAAAAAGCCCAATCCCAACAAACCCA.....GACCCCAAC 15687
290 hrThrSerValLeuIleArgLysTyrAlaIleGlyAspTyrSerLysLeu 306
   |||
   |||.....:|||||:|||||
15688 .....TCAAGTACG 15696
307 LeuGluGlyAlaThrLeuGlnLeuThrGlyAspAsnValAsnSerPheG1 323
   |||
   |||.....:|||||:|||||
15697 CTAGAAGCGCGGCTTTATGCTGAGCGGCGCATGAGCTG..... 15735
323 nAlaIleValPheSerSerAsnAspIle.....G 333
   |||
   |||.....:|||||:|||||
15736 ..CGGGTAAATTTTATCCAAAGAACGACGACCACTTTGTGCTTTGGTG 15784
333 LylGluArgIleGluIleuSerAspGlyThrTyrThrLeuThrGluLeuAsn 349
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   |||.....:|||||:|||||
15785 GCAAAGGACACAAAACGACCGCACTGTGCGCACAAAAACGGTGATTTT 15834
350 SerProAlaGlyTyrSerIleAlaGluProIleThrPheLysValGluAl 366
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   |||.....:|||||:|||||
15835 AGT...ACAGGATTTGAA.....AAACCCACACCAAGCTTGTGGCAA 15875
366 aGlyLysValIlyrThrIleIleAspGlyLys.....GlnIleG 379
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   :|||||.....:|||||:|||||
15876 TGAAGGATTTGGTACCACTTATTTAGCGGTAAAGAAATGAATGATGAAGCA 15925
379 LAsnProAsnLysGluIleValGluProTyrSerValGluAlaTyrAsn 395
   |||
   |||.....:|||||:|||||
15926 ATATATCAATTGCAAGATGAACATGTCGCCCTGTCACTGAATATTAAGAAATATAT 15975
396 AspPhe.....GlnGluPheSerVal 402
   :|||||
   :|||||.....:|||||:|||||
15976 GATATATATTTATGACAGACCAACAACAATTCACCAAAAAAATATAAGC 16025
402 lleuThrThrGlnAsnTyrAla.....LysPheTyrT 413
   :|||||
   :|||||.....:|||||:|||||
16026 CAGCGCGCAAAAAAACCCCTGCTTATTTGGTCAGCATGATGAATAGTTTATTT 16075

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413	yr.....	Alblys.....	Asnlysasn gly	419
	::			
16076	TTATATGTAAGTACTTATATGACTTATGACATTCACCAAGCAAAAGCAAGCTTGCT			161255
420	SerSerGlnValValIyrCysPheasnAlaAspLeuLysSerProProAs			436
		:::		
16126	GTTCTCCCAAGATPACCAAGCACCATAAGAAATATTTTGGCTAAATPACCCAGA			16175
436	pSerGlnAspGlyGlyLysGlyThrMetThrProAspPheThr.....			450
	:::			
16176	TGGC.....	AAAGTAAGCAGACAGACAATAAAGTTACCAGAAATG		16213
450			450
16214	TTCTACAAAGCCAAAGATAAGCCGTATACCCGATTCATGCCAAAAAGC			162635
451	GlyGluValLysTyrrThHisIleAlaGlyAr		461
16264	TATGACCACATCAGATTGTTGGTGAAGTATGTATATGATACAAAGGCA			16313
461	gaSPLeuPheLysTyrrThValLysProArGAspThrAspProAspThr			478
	:::			
16314	CCCAACACCGCATTAATTTGTGTCAAGCGCGTCAAGCGATGTCACTACTC			163635
478	heLeuLys.....			481
	::			
16364	AGCTGCCAGTCGAGTAAATTCACCTTAATATGCTTTGGCGAGCTAC			16413
482	IleLysLysValIleGluLysGlyTyrrArgGlyLysGlyGlnAlaIleG			498
	:::			
16414	CTGACCCACAAAAAAGACAAAGGTATATACAAAGATGAGATGCATCA			164635
498	uTyrrSerGlyLeuThrGluThrGlnLeuArgAlaIaIaThrGlnLeuAla			515
	:::			
16464	GCAAAAAGCTCTTAAGAT.....			16482
515	LeTyrrTyrrPheThr.....	AspSerAlaGluLeu		524
	:::			
16483	..TATATATTGACCAAGACTTTATCCACAGATGAGCATGACGANTGC			16530
525	AspLysAspLysLeu.....	LysAspTyrrHi		533
	:::			
16531	GATGACGATATAGTTTGACCCGATCTGTATGCACAAAGATGATAAATACA			16580
533	scGlyPheGlyAspMetLAsnSerThrIleuAlaAlaLysIleLeu			550
	:::			
16581	TGGCGATGATGATTTG.....	ATTGCAT		166035
550	alGluTyrrAlaGlnAspSerAsnProGlnLeuThrAspLeuAspHe			566
	:::			
16604	CTGATATTCACAAAGATGATGACGCCGAGATGGCGATGACATTCACATGAT			166535
567	PheIleProAsnAsnAsnLysTyrrGlnSerLeuIleGlyTyrrGlnTyrrHi			583
	:::			
16654	TTTG.....	GGTGATGTGCAGATGTGACGCCGACGAGCAAGTAGTATCA		166975
583	sProGluAspLeuValAspIleLeuArgMetLysPylsGlyValI			600
	:::			
16698	TGCAGGTAAAT.....	ATTGCCCCCTTAATTTGAAAACAAAATACT		167355
600	LeProVal.....	ThrHisAsnLeuThrLeu.....		608
	:::			
16736	TGGCCATTATATGAGCTACTCATGAAAAAACCTTTGGCCCTAATGTGTA			167855
609	ArgLysThrValThrGlyLe		615
	:::			
16786	AATTAAGCTAAGTTGATGATAAATTTGCACCAACACAGCCTTAATCGTAA			168355
615	uAlaGlyAspArgTyrrLysAspPheHisPheGluLeuGlyLeuLysAsn			632
	:::			
16836	ATTAAACGTATGAGAGAGTGATATTCGCTTTGATATATTC.....	AAAAATG		16879


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6898 AATGAAAAAGGACGCTT.....GTAACAGGAGA 6926
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317 pAsnValAsnSerPheGlnAlaGValPheSerAsnAspIleGly 334
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6927 CGCTGTTAAATATAC.....ACTGTAAGTAAACAGGAAGATGAT 6967
      :::::  :::::  ::  |||
334 LuArgIleGluLeuSerAspGlyThrTyThrLeuThrGluLeuAsnSer 350
      :::::  :::::  ::  |||
6968 TCGATTACAGTTAATGAT.....GATATTAAATAGT 6999
      :::::  :::::  ::  |||
351 ProAlaGlyTyrSerIleAlaGluProIleThrPheLysValGlu...Al 366
      |||  |||  :::::  :::::  ::  |||
7000 .....GCTTATGTGATTACATAAACCAGGCCAAC 7031
      :::::  :::::  ::  |||
366 aGlyLysValTyrThrIleIleAspGlyLysGluIleGluAsnProAsnL 383
      :::::  :::::  ::  |||
7032 TAAATAAGTT.....ATGAGAGATGAAAA...GTAAAAAT 7065
      :::::  :::::  ::  |||
383 ySgLIleValGluProTyrSerValGluAlaTyrAsnAsp..... 396
      ::|||  |||  |||
7066 .....AAAGTTACGCTGATTAATGATTCAAGTAA 7095
      ::|||  |||  |||
397 .....PheGluGluPheSerValLeuThrThrGlnAsnTy 408
      |||  :::::  :::::  :::::  ::  |||
7096 GAAATGACAGCTTCAACAGCAAAATATTATTAATCTAATAATA 7145
      |||  :::::  :::::  :::::  ::  |||
408 rAlaLysPheTyrTyThrAlaLysAsnLysAsnGlySerSerGlnValT 425
      |||  :::::  :::::  :::::  ::  |||
7146 AGCTGAACAATAATTAAAGCAAAACAACTGGACAAATTATATGAA 7195
      |||  :::::  :::::  :::::  ::  |||
425 yRcYpHeAsnAlaAspLeuLysSerPro.....ProAspSerGluAsp 439
      |||  |||  :::::  :::::  ::  |||
7196 ATAATAACAATATCCATTAAACACGCGATTATTACGACACCTTGAT 7245
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440 GlyLysThrMetThrProAspPheThrThrGlyLysValLys..... 454
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7246 CATGTGATATCAATTAAGATTAAGAACTA...GAATTAAGACGG 7292
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455 ...TyThrHisIleAlaGlyArgAspLeuPheLysTyThrValLysP 470
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7293 AAATTAATACCTTCACGTGGAGCTGAC..... 7320
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470 rOArgAspThrAspProAspThrPheLeuLysHisIleLysValIle 486
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7321 .....TAAGTTTAGATGATACA 7338
      ::|||  |||  |||
487 GluLysGlyTyrArgGluLysGlyGlnAlaIleGluTyrSerGlyLeuTh 503
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7339 GATTAAGGCTCAAAATTAATAGTATAGTCAGTCATATATATGAC 7388
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503 rGluThrGlnLeuArgAlaIleThrGlnLeuAlaIleTyrTyRphethra 520
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7389 AAAGACA.....TTAGTCGTAAATAATACGACAG 7417
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520 sPseSerAlaGluLeuAspLysAspLysLeuLys.....AspTyr 532
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7418 AC.....TTTGATTATACAAAGCTAGAAAGTGTAAACCTTCATT 7458
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533 HisGlyPheGlyAspMetAsn.....AspSerThrLeuAlaIle 545
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7459 AAAAATACAGTACCTTCTTGATAGTATAGCATTCATATCCACAATC 7508
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545 lAlaLysIleLeuValGluTyrAlaGlnAspSerAsnProGlnLeuT 562
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7509 AAAATAAGTTAGACCTAATTCGATTCGATAC..... 7542
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562 hrAspLeuAspPhePheIleProAsnAsnAsnLysTyrGlnSer..... 576
      |||  |||  |||  |||  |||
7543 .....TTCACAAAGCAATGTTAATAATACGCTTCTTATAAC 7581
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577 .....LeuIleGlyThrGlnTyrPHisProGln 585
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7582 GCCCAAGCAAGAAATTAATCTGATTAATAGGCTTAACTAATAATATGT 7631
585 uAspLeu.....ValAspIleIleArgMetGluAspLysL 597
      :::::  ::|||  |||  |||  |||
7632 TGAGATTAAAGATCCTTATGTTATAGACGTATA.....CAGATTAAC 7675
      ::|||  |||  |||  |||  |||
597 ySgLIleValIleProValThrHisAsnLeuThrLeuArgLysThrValThr 613
      ::|||  |||  |||  |||  |||
7676 AAAAGTTAGTGCCT.....GATTCATTGAAGTGGCGGATATGATTTTA 7719
      ::|||  |||  |||  |||  |||
614 GlyLeuAlaGlyAspArg.....ThrLysAs 622
      ::  |||  |||  |||  |||
7720 AATGGAATTCCTGATTAATATGCAACACCTGTATGCTGATACCACTGAGA 7769
      ::  |||  |||  |||  |||
622 pPheHisPheGluIleGluLeuLysAsnAsnLysGlnLeu..... 636
      ::|||  |||  |||  |||  |||
7770 ATATGCACTTGAGAACCTACAGAGAACAAATAAACCCTTAAGGTTTC 7819
      ::|||  |||  |||  |||  |||
637 ...LeuSerGlnThrValLys..... 642
      ::|||  |||  |||  |||  |||
7820 ATTTCAAACAAATCAATTAATACCTTACTATATTATCTTAAACAAGC 7869
      ::|||  |||  |||  |||  |||
643 .....ThrAspLysThrAsnLeuGluPheLys 651
      |||  |||  |||  |||  |||
7870 CTGATGTGTAACCTATATCCAGGCAACCTACAAAAAGAGGAGATTAA 7919
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651 sAspGlyLysAlaThrIleAsnLeuLysHisGlyGluSerLeuThrLeug 668
      |||  |||  |||  |||  |||
7920 AGATGGCTCTAAATTCGTAAACACCTTACAGGTGCACCT..... 7959
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668 lngLysLeuProGluTyrSerTyrLeuValLysGluThrAspSerGlu 684
      ::|||  |||  |||  |||  |||
7960 ...CAGTAATAAAGTGGCAGCTTCGTACTAAAGAGCTGTGCACAC 8007
      ::|||  |||  |||  |||  |||
685 .....GlyTyrLysValLysValAsnSerGlnGluValAlaAs 697
      ::|||  |||  |||  |||  |||
8008 GACAACATTAATTAATGAGATGCAATTAACGAACCA..... 8049
      ::|||  |||  |||  |||  |||
697 nAlaThrValSerLysThrGlyIleThrSerAspGluThrLeuAlaPheG 714
      ::|||  |||  |||  |||  |||
8050 ...TCAACCATTCAGATGCCGTGTAAACAGATGACCAAC.....G 8089
      ::|||  |||  |||  |||  |||
714 LuAsn.....AsnLysGluProValIleProThrGlyVal 725
      |||  |||  |||  |||  |||
8090 AAATACAGTAAATGTGGAAGATTCATTCATTAATCTAATCAACTGT 8139
      |||  |||  |||  |||  |||
726 Asp 726
      |||
8140 GAT 8142

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seq_documentation_block:
? Sequence 368, Application US/60068139
? GENERAL INFORMATION:
? APPLICANT: LAGACE, ROBERT E.
? APPLICANT: CORLEY, NEIL C.
? APPLICANT: RUSSO, FRANK D.
? APPLICANT: HANN, AMY L.
? APPLICANT: HEATH, JOE D.
? APPLICANT: FINNEY, GREGORY L.
? TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS
? TITLE OF INVENTION: GENOME, FRAGMENTS THEREOF, AND USES THEREOF
? NUMBER OF SEQUENCES: 471
? CORRESPONDENCE ADDRESS:
? ADDRESS: INCYTE PHARMACEUTICALS, INC.
? STREET: 3174 PORTER DRIVE
? CITY: PALO ALTO
? STATE: CALIFORNIA
? COUNTRY: USA
? ZIP: 94304
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk

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;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/60/068,139
; FILING DATE: HEREWITH
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PM-0008-2 P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ. ID NO.: 368:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14346 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: genomic DNA
; IMMEDIATE SOURCE:
; CLONE: MCALC368
;
; US-60-068-139-368

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alignment_scores:
  Quality: 169.50      Length: 864
  Ratio: 0.479        Gaps: 42
  Percent Similarity: 40.972  Percent Identity: 19.444

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  US-09-494-297-2 x US-60-068-139-368 ..

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Align seg 1/1 to: US-60-068-139-368 from: 1 to: 14346

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558 CCATCAGCAGTGATGACATTCAC.....CACCTTATTTTGATAAAATTC 601
23 rLysArgPheThrVal.....ThrLeuValGlyValPheLeuMet 37
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602 CCCAAATATCCGATCTGCACCTGAGAAAACAGCGAGCATGTGTTGATGC 651
37 lePheAlaLeuValThrSerMetValGlyAlaLysThrValPheGlyLeu 53
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652 TAAAAAAGCAATATACATCC.....AAATATATGTTAT 686
54 ValGluSerSerThrProAsnAlaIleAsnProAspSerSerSerGluTy 70
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687 GGTGCATTTGTCATCACTT..GCCAAAACCCA.....ACCTA 721
70 rArgTrpTyrGlyTyrGluSerTyrValArg.....GlyHisP 83
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
722 CATGAAATATCAACAGAACAAAACATCAAAAACAAAACAGCGCATG 771
83 rArgTrp.....TyrLysGlnPheArgValAlaHisAsp 93
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
772 ATATCAAAACATTCGTTTGGCTATATGAGCTAAGA.....GAG 812
94 LeuArgValAsnLeuGluGlySerArgSerTyrGlnValTyrCysPheAs 110
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
813 CTGAGCCTAATAAATAAAAGTGCA..... 836
110 nLeuLysLysAlaPheProLeuGlySerAspSerSerValLysLysTrp 127
836 ..... 836
127 rLysLysHisAspGlyLysSerThrLysPheGluAspTyrAlaMetSer 143
836 ..... 836
144 ProArgIleThrGlyAspGluLeuAsnGlnLysLeuArgAlaValMetTy 160

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837 .....GACACCCAGAGGACAGACAGACCGTCGCATCATTTT 871
160 rAsnGly.....HisProGlnAsnAlaAsnGlyIleMetG 172
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872 CACCACACCTACTTATTTATTCATGAGTGAATGCCAGACCACTATGCG 921
172 LysGlyLeuGluProLeuAsnAlaIleArgValThrGlnGlnAlaValTrp 188
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
922 CA.....AAGCGGGTAAATTGACTGTAGGGCAATGG 956
189 TyrTyrSerAspAsnAlaPro.....IleSerAsnProAspGly 201
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
957 TTGTATCTGACCGATGTCGCAAAAACGCCCATTTTATGATTAACAGACGA 1006
201 u.....SerPheLysArgGluSerGluSerAsnL 211
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1007 TAAAGTAGGACACTTATTTTAACTCAACCAAGAAATCAAAAGAGCGATT 1056
211 euValSerThrSerGlnLeuSerLeu.....MetArgGlnAlaLe 224
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1057 TGGTGAATGACGACACATTTATCTAACAGCTTAATATAACACACC 1106
220 .....MetArgGlnAlaLe 224
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1107 CCGGCACACTTATAGCGTGACCTTTGATCAAAATACCTAAAGGCAAAAT 1156
224 uLysGlnLeuIleAspProAsnLeuAlaThrLysMetProLysGlnValP 241
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1157 GCTTTATTTATGACACCAACCAACAGCAACAGCCGATGGCGTTATATCA 1206
241 roAspAspPhe.....GlnLeuSerIlePheGlu 250
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1207 GAAGTCAGTTTGTATACCGACAAAAGGTCAATGAGCGCATGTCTATAG 1256
251 SerGluAspLys.....GlyAspLysTyrAsnLysGlyTyrGlnAsnLe 265
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1257 ATTGACGCCAAGATTATGCGAACCGCTTACTGCGCACACCAAAATCTT 1306
265 uLeuSerGlyGlyLeu.....ValProThrL 274
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1307 GATTGATGATTAACCAATACCGACCTTTGTTTAAGACGTGTTCTCCA 1356
274 yspProProThrProGlyAspProPheMetProProAsnGlnProGlnThr 290
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1357 AAAAAGCCATCCCAACACCA.....GACCCCAAC..... 1388
291 ThrSerValLeuIleArgLysTyrAlaIleGlyAspTyrSerLysLeuLe 307
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1389 .....TCAGATACGCT 1399
307 uGluGlyAlaThrLeuGlnLeuThrGlyAspAsnValAsnSerPheGlnA 324
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1400 AGAAGCGCGGCTTTTATGCTGAGTGCGGAGTAGACTG.....G 1437
324 laArgValPheSerSerAsnAspIle.....Gly 333
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1438 CGGTAATTTTATTCATGACAAACCACTTTTGTGCTTGTGGTGGC 1487
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1488 AAACGAGACAAAACGACGCAACCTGTCGCCCAAAAACGGGTGATTTTAA 1537
350 rProAlaGlyTyrSerIleAlaGluProIleThrPheLysValGluAlaG 367
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1538 T...ACAGGATTGAA.....AAACCCAGACACAGCTTTGTTGGCATG 1578
367 LysValTyrThrIleIleAspGlyLys.....GlnIleGlu 379
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1579 AAGGATTTGGATGATTTATGACGTAAAGTTAATGATGAAGTCAAT 1628
380 AsnProAsnLysGluIleValGluProTyrSerValGluAlaTyrAsnAs 396
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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3371 CTAAGTTCAGGTCAAGAT.....ACACAGATTATGTT.....GCT 3408
663 GluSerLeuThrLeuGlnGlyLeuProGluGlyTyrSerTyrLeuVally 679
3409 GATTCGTGGAAA.....CCAGAA.....GATTAATTCGTTTC 3440
679 sGluThrAspSerGluGlyTyrTyrLysVal.....LysValAsnSerG 693
3441 ACCGACAGCAGCAAAACAGGTCAAGAGCTTCGCTTGGAATAAATTGATGTC 3490
693 InGluValAsnMetThrValSerTyrTnGlyTyrIleThrSerAspGlu 709
3491 AGGGAACAGTCAAT.....GTTGATTAATAAAGCC.....GATTAT 3525
710 ThrLeuAlaIlePheGluAsnAsnLysGlu 718
3526 GAATATGCTCATTAATAAATGGCAAAAAA 3552

